

ON THE IMPOSSIBILITY OF CONSTRUCTING GOOD POPULATION MEAN ESTIMATORS IN A REALISTIC RESPONDENT DRIVEN SAMPLING MODEL

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Current methods for population mean estimation from data collected by Respondent Driven Sampling (RDS) are based on the Horvitz-Thompson estimator together with a set of assumptions on the sampling model under which the inclusion probabilities can be determined from the information contained in the data. In this paper, we argue that such set of assumptions are too simplistic to be realistic and that under realistic sampling models, the situation is far more complicated. Specifically, we study a realistic RDS sampling model that is motivated by a real world RDS dataset. We show that, for this model, the inclusion probabilities, which are necessary for the application of the Horvitz-Thompson estimator, can not be determined by the information in the sample alone. An implication is that, unless additional information about the underlying population network is obtained, it is hopeless to conceive of a general theory of population mean estimation from current RDS data.

1. Introduction. Obtaining useful samples of *hidden* populations *with a network structure* is a prerequisite for many types of research, especially for studies of epidemiological problems such as addiction and HIV/AIDS. Respondent Driven Sampling (RDS) is a recently proposed sampling technique that seeks to sample from such hidden populations in a way that allows for valid estimation of population quantities.

RDS begins with a non-random selection of a small set of individuals in the target population. These individuals are referred to as *seeds*. Data relevant to the study is first collected from these seeds. In addition, the seeds are asked to report their degree. We follow Volz and Heckathorn (2008) and define the degree of an individual as the number of people that the individual could, in principle, recruit. The seeds are then asked, and provided financial incentive, to recruit into the study their social contacts (provided the contacts are also in the target population). The sampling continues in this way with newly recruited sample members recruiting the next wave of sample members until the desired sample size is reached. Whenever a subject comes into the study, data relevant to the study are collected from him/her

and in addition, his/her degree in the target population is recorded. Further, a record of who recruited whom is maintained.

While RDS has proved to be extremely effective at penetrating hidden populations, the statistical dependencies that it induces in the sample make the problem of estimating population quantities an intricate task. Let us now define basic notation to describe the current employed methods of estimation from RDS data. Let G denote the population equipped that we wish to sample from. We assume that G has a network/graph structure with nodes/vertices representing and edges/connections representing extant social relationship. In particular, the neighbors of an individual denote the set of subjects that the individual can potentially recruit. Let y denote a population quantity whose mean, μ , we are interested in estimating. A sample of size n is drawn via RDS from G . Some of the individuals in the sample are selected as seeds while the others are selected through the process of recruitment as described above. From each of the sample individuals, data on the population quantity y is collected. Also, the population degrees of the sample individuals are obtained by enquiry and the information on recruitment (i.e., who recruited whom) is recorded. The goal is to estimate μ using all available information i.e., the y -values of the sample individuals y_1, \dots, y_n , the population degrees of the sample individuals d_1, \dots, d_n and the information on who recruited whom.

The current methods of estimation from RDS data, developed mainly in Heckathorn (1997), Heckathorn (2002), Salganik and Heckathorn (2004), Volz and Heckathorn (2008) and Gile (2010) can all be viewed as being based on the Horvitz-Thompson estimator (Horvitz and Thompson, 1952), which is a standard estimator in the theory of survey sampling. The Horvitz-Thompson estimator for the population mean μ is given by

$$(1) \quad \hat{\mu}_{HT} := \frac{\sum_{i=1}^n y_i / \pi_i}{\sum_{i=1}^n 1 / \pi_i},$$

where π_i is known as the inclusion probability of the i^{th} sample individual and is defined as the probability that the i^{th} sample individual is included in the sample. This estimator is applicable to both with replacement and without replacement sampling models.

It should be noted that the Horvitz-Thompson estimator is applicable only to probability sampling schemes where the inclusion probabilities π_1, \dots, π_n of the sample individuals can be determined. In the papers cited above, the authors place a variety of assumptions on the RDS data generation process and argue that, under those assumptions, the sample obtained according to RDS can be taken to be a probability sample and that, as required by the

Horvitz-Thompson estimator, that the inclusion probabilities of the sample individuals can be determined as a function of their self-reported degrees. We shall describe here the methods of Volz and Heckathorn (2008) and Gile (2010). The estimator in Volz and Heckathorn (2008) is termed RDS II and, as illustrated in Gile and Handcock (2010), is an improvement over the classical RDS estimation procedure developed in Heckathorn (1997), Heckathorn (2002) and Salganik and Heckathorn (2004). As a result, these earlier estimators no longer need to be considered.

Volz and Heckathorn (2008) assume that respondents recruit uniformly at random from their network neighbors (this ensures that RDS is a probability sampling model). In addition, they also make the following pair of assumptions:

1. Samples are drawn *with-replacement*
2. Each respondent recruits exactly one other respondent into the study.

Volz and Heckathorn (2008) argue that under these assumptions, the process of obtaining an RDS sample is equivalent to performing a random walk on the population network. They then assert, based on convergence properties of Markov chains, that the inclusion probability, π_i , of the i th individual in the sample should be directly proportional to his/her degree, d_i . They therefore construct their estimator for the population mean μ by replacing π_i in the formula (1) by d_i . This leads to the intuitively appealing and mathematically uncomplicated estimator RDS II where the population mean is estimated by the weighted average of the sample observations, the weights being inversely proportional to the self-reported population degrees of the sample individuals.

The problem, however, with RDS II is that it is founded on the two assumptions 1 and 2 which are both routinely violated in practice. Assumption 1 which implies that any individual may be recruited into the sample more than once, is never allowed. Assumption 2 can be relaxed (see Salganik and Heckathorn (2004, pp. 210)) to the case where all respondents recruit an equal number of respondents. In practice, however, different respondents recruit differently (we shall refer to this as differential recruitment in the sequel) and this aspect is not taken into account by Volz and Heckathorn. More details on the violation of these assumptions in real-world sampling can be found in Heimer (2005).

Regrettably, when assumptions 1 and 2 are violated, the underlying theoretical foundation for RDS II breaks down making its role as a population mean estimator unsound and suspect. Indeed, if the samples are drawn without replacement, then the recruitment process is no longer Markov because,

in standard and near-universal practice, it is not allowed to re-recruit an individual who is already in the sample (however distant past he/she may have been recruited in) and thus the process is forced to have memory.

The estimation procedure of Gile (2010) is much more elaborate compared to RDS II. Gile (2010) assumed that the underlying data collection process in RDS can be modeled as a *successive sampling* process. Under the assumption of successive sampling, Gile described an iterative algorithm for approximating the inclusion probabilities π_i based on the information contained in the RDS sample alone. The algorithm, which can be considered as a variant of the Expectation-Maximization (EM) algorithm (see Gile (2010, pp. 12)), further assumes that the population size is known and also makes an assumption on the graph structure of the true population (a variant of the configuration model for networks).

Just like the assumptions of Volz and Heckathorn, the assumption of successive sampling is also not realistic and would not be a reasonable approximation to most real-world RDS data collection processes. For example, although it allows for without-replacement sampling, it still does not allow for differential recruitment. Unfortunately, the estimator of Gile (2010) crucially depends on the assumption of successive sampling and it is not at all clear as to how it can be extended to real-world situations where the assumptions of successive sampling do not hold.

To illustrate the divergence of the assumptions of Volz and Heckathorn (2008) and those of Gile (2010) with real world RDS sampling, we will review a recent study of the HIV epidemic in St. Petersburg, Russia. A primary objective of *The Sexual Acquisition and Transmission of HIV Cooperative Agreement Project* (SATHCAP) study was to estimate certain population means (including the prevalence of HIV and hepatitis C) in the population of Injection Drug Users (IDUs) in St. Petersburg. In the first cycle of recruitment conducted from November 2005 through December 2006, a sample of 373 IDUs was obtained using an RDS design and data on variables relevant to the study (for example, HIV status, Hepatitis C status etc) were collected from the subjects. In addition, their self-reported population degrees were recorded. The histogram of these self-reported degrees in the SATHCAP dataset is given in Figure 1.

The SATHCAP sample was collected without replacement and different individuals recruited differently even though each individual received the same fixed number of coupons. We have displayed this differential recruitment pattern in Table 1. It is clear from Table 1 that the assumptions of Volz and Heckathorn (2008) and those of Gile (2010) are violated for the SATHCAP dataset.

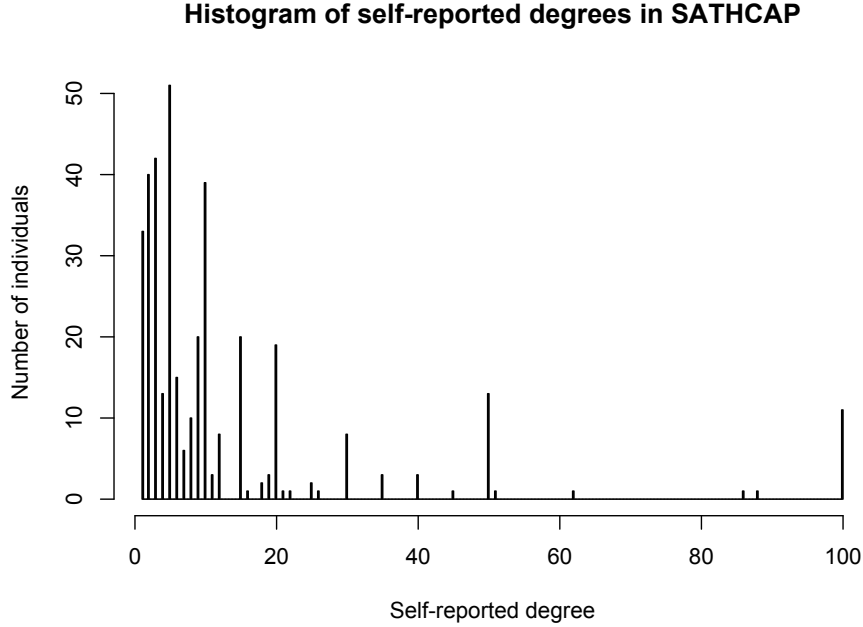


Fig 1: Histogram of the self-reported degrees in the SATHCAP dataset.

The goal of this paper is to argue that for *realistic* RDS sampling models, it is impossible to determine the inclusion probabilities π_1, \dots, π_n from the information available in an RDS sample. The determination of inclusion probabilities is possible only under highly simplistic modeling assumptions such as those made by Volz and Heckathorn (2008) or Gile (2010).

In section 2 of this paper, we shall describe a realistic RDS sampling model, to be denoted by \mathcal{M} , that will account for both differential recruitment and sampling without replacement, thus creating a more faithful approximation to the data collection process in the SATHCAP study. The model \mathcal{M} is conceptually uncomplicated, although it is more elaborate than currently studied RDS models since both without replacement sampling and differential recruitment are assumed. Two main features of \mathcal{M} are: (a) respondents recruit only from those of their neighbors who are not already in the sample, and (b) instead of recruiting exactly one other subject, each respondent recruits no other subject with a certain probability, exactly one other subject with a certain probability and so on. We assume that these probabilities (which will be *parameters* in the model) are the same for all

Percentage of Subjects	Number of Recruits
58.98	0
15.55	1
10.19	2
9.65	3
3.49	4
1.34	5
0.8	6

TABLE 1

Observed Recruitment Pattern in SATHCAP. 58.98% of the sample individuals did not recruit others into the study (in spite of receiving coupons), 15.55% of the individuals recruited exactly one other individual into the study etc.

the respondents. We refer the reader to section 2 for a full description of the model.

In order to use the Horvitz-Thompson estimator for estimating μ from data generated according to the model \mathcal{M} , it is necessary to determine the inclusion probabilities π_1, \dots, π_n under \mathcal{M} . The behavior of the inclusion probabilities under \mathcal{M} is quite detailed involving both individual degrees and the overall network structure. In section 3, we demonstrate that, in contrast to the RDS models studied so far in the literature, the model \mathcal{M} is such that the inclusion probability for an individual depends not only on his/her degree but also on the network structure of the population. We present two simulated population networks having *identical degrees* but very different inclusion probabilities under our sampling model.

Our example demonstrates that the inclusion probabilities π_1, \dots, π_n for a realistic RDS model depend not only on the population degrees of sample individuals, d_1, \dots, d_n but also on other characteristics of the underlying population graph. Since the self-reported degrees d_1, \dots, d_n present the only information about the population network that is contained in an RDS sample, we deduce that the inclusion probabilities π_1, \dots, π_n for realistic RDS models can not be calculated from the RDS sample. This precludes the application of the Horvitz-Thompson estimator as a population mean estimator from RDS data. As a result, a general estimation theory is not possible from RDS data.

The situation can only be remedied if one obtains additional information about the underlying population through an RDS sample. We have some incomplete ideas in this regard that we describe in Section 4. We organize concepts as follows: in the next section, we describe our RDS sampling model \mathcal{M} . In Section 3, we show that inclusion probabilities under \mathcal{M} depend not only on the degrees but also on the structure of the underlying population

network. We finish the paper summarizing our conclusion and describing some ideas for future work.

2. A Realistic Respondent Driven Sampling Model. In this section, we describe a new model for RDS, to be denoted by \mathcal{M} , that allows for both without replacement sampling and differential recruitment. As explained in the previous section, it is inspired from the underlying data collection mechanism in the SATHCAP study.

Our model \mathcal{M} is conceptually simple. We consider nonnegative real numbers p_0, p_1, p_2, \dots that sum to 1 and instead of supposing that every respondent recruits exactly one other subject, we assume that each respondent decides to recruit no other subject with probability p_0 , exactly one subject with probability p_1 , exactly two subjects with probability p_2 and so on. This would clearly permit differential recruitment. Suppose that a respondent decides to recruit s_1 subjects and suppose that the number of his/her neighbors that are not already in the sample is s_2 . We then assume that the respondent actually recruits $\min(s_1, s_2)$ subjects *uniformly at random* from among his/her neighbors who are not already in the sample. As a consequence of this assumption, respondents recruit only from those of their neighbors that are not already in the sample. Therefore, \mathcal{M} rules out subjects reappearing in the sample and hence, is a without-replacement sampling model.

We assume that seeds are chosen uniformly at random from all the population members who are not already in the sample. The other assumption that is commonly made concerning seed selection in standard RDS analysis is that seeds are chosen with probabilities proportional to degrees. It is debatable as to which assumption (uniformly at random or random with probabilities proportional to degrees) is more reasonable. We also assume that the sampling starts with one seed and that new seeds are selected only when necessary i.e., only when recruiting stops.

The following is the complete description of the sampling model in the form of a randomized algorithm. The set *active* represents active/potential recruiters i.e., the sample individuals who currently possess coupons and who can therefore potentially recruit other individuals into the sample. When there are multiple active recruiters, we assume that one of them (uniformly at random) recruits first.

1. Initially there are no active recruiters. So we initialize *active* to be the empty set. The following steps are then repeated till the desired sample size n is reached.
2. If *active* is empty, we need to select a seed. The seed is chosen from the set of all population nodes that are *not* already in the sample and

the seed is included in both the sample and the set *active*.

3. If *active* is non-empty, i.e., if there are active recruiters, the following steps take place
 - (a) One node is chosen uniformly at random from *active*, this respondent recruits first. Let *available* be the set of all neighbors of this node that are NOT already in the sample and let s_1 be the size of *available*.
 - (b) A number s_2 from $0, 1, \dots$ is chosen with probabilities p_0, p_1, \dots . Then $\min(s_1, s_2)$ nodes are chosen from *available*. These nodes are included in the sample and in the set *active*. Also the recruiter is deleted from *active*.

This completes our description of \mathcal{M} . For every sampled individual, we collect data on the study variables and his/her degree (self-reported). The probabilities p_0, p_1, \dots are parameters in \mathcal{M} .

In the next section, we demonstrate that for \mathcal{M} , the inclusion probability of an individual depends crucially on the population graph structure and that the inclusion probabilities can not be determined by the degrees alone.

3. Inclusion probabilities under the model \mathcal{M} . In this section, we argue that, for the sampling model \mathcal{M} , the inclusion probabilities of individuals depend not only on their degree but also on the network structure of the true population. We proceed by constructing two population networks G_1 and G_2 having the same nodes (say, N , of them) and having identical degrees but vastly different inclusion probabilities under the model \mathcal{M} . We would like to stress that the two networks G_1 and G_2 have identical degrees; not just identical degree distributions. In other words, both G_1 and G_2 have the same set of nodes, which can be numbered $1, \dots, N$, and, for each $i = 1, \dots, N$, the degree of the i th vertex is exactly the same in both G_1 and G_2 .

We base our construction of the networks G_1 and G_2 on the degrees reported by the 373 individuals in the SATHCAP sample (see Figure 1). We take these 373 self-reported degrees and resample from this set uniformly with replacement to create a set of N integers, where $N > 373$ will be specified shortly. Let us denote this set of N integers by D_1, \dots, D_N and we assume that $D_1 \geq D_2 \geq \dots \geq D_N$. A standard result (see, for example, Sierksma and Hoogeveen, 1991) asserts that there exists a graph on N nodes with degrees D_1, \dots, D_N (in which case, D_1, \dots, D_N is known as a *graphical*

sequence) provided the following criterion is satisfied:

$$(2) \quad \sum_{i=1}^k \max(D_i - k + 1, 0) \leq \sum_{i=k+1}^N D_i \quad \text{for every } k = 1, \dots, N-1.$$

Now because the integers D_1, \dots, D_N have been constructed from the SATH-CAP self-reported degrees (which have the histogram given in Figure 2), the histogram of D_1, \dots, D_N will also approximately (at least when N is large) be as in Figure 2 (with just a change of scale on the y -axis). As a result, it is not hard to see that, when N is large, the probability that there exists a graph with degrees D_1, \dots, D_N is quite high (mainly because the right hand side of (2) increases with N while the left hand side remains unchanged). We choose $N = 5000$ and, at least in simulations, this invariably resulted in a graphical sequence D_1, \dots, D_N .

For such a fixed graphical sequence D_1, \dots, D_N , we construct networks G_1 and G_2 having N nodes with degrees D_1, \dots, D_N . Let us first describe the construction of G_1 . G_1 is a deterministic graph with degrees D_1, \dots, D_N . We take the algorithm for the construction of G_1 from Raman (1991). The algorithm starts with the empty graph (the graph on N nodes with no edges) and adds edges until the i th node has degree D_i for all $i = 1, \dots, N$. At any stage of the algorithm, the residual degree of the i th node is defined as the difference of D_i and its current degree. The algorithm proceeds by repeatedly joining the node with the largest residual degree (say, k) to the k nodes with the next largest residual degrees. It can be shown, see Raman (1991), that, whenever D_1, \dots, D_N is graphical, this algorithm results in a graph with degrees D_1, \dots, D_N . From the construction, it is easy to see that G_1 is a deterministic graph in which the high degree nodes have a tendency to connect to other high degree nodes. In other words, there is a *homophily* (the tendency of individuals to associate with those similar to themselves) by degree in the network G_1 .

Let us now explain the construction behind G_2 for which we take the randomized algorithm of Bayati, Kim and Saberi (2007, pp. 329, Procedure A). This algorithm also starts with the empty graph and sequentially adds edges between pairs of non-adjacent nodes until the i th node has degree D_i for all $i = 1, \dots, N$. Unlike Raman's algorithm however, this is a probabilistic algorithm and at every step, the probability that an edge is added between two non-adjacent nodes i and j is proportional to

$$R_i R_j \left(1 - \frac{D_i D_j}{2(D_1 + \dots + D_N)} \right),$$

where R_i is the residual of node i . Bayati, Kim and Saberi (2007) showed that, provided that D_1 (which is the maximum of D_1, \dots, D_N) is sufficiently small compared to $D_1 + \dots + D_N$, this algorithm produces a random graph with degrees D_1, \dots, D_N with high probability and, moreover, the distribution of this random graph will be approximately uniform on the set of all graphs with degrees D_1, \dots, D_N . This condition on D_1, \dots, D_N is satisfied in our case and we can thus view G_2 as one realization of a random graph with degrees D_1, \dots, D_N whose distribution is approximately uniform over all graphs with degrees D_1, \dots, D_N .

We have thus created two networks G_1 and G_2 on N nodes having identical degrees D_1, \dots, D_N . However, these two networks are very different from each other. G_1 is a deterministic graph with a strong homophily by degree. On the other hand, G_2 is one realization of a random graph that is uniformly distributed over all graphs with degrees D_1, \dots, D_N . We now show that the inclusion probabilities of the nodes $1, \dots, N$ for a sample of size $n = 373$ (we use $n = 373$ because that was the sample size in the SATHCAP study) drawn according to the realistic RDS sampling model \mathcal{M} are vastly different for the two networks G_1 and G_2 .

From each of G_1 and G_2 , we obtained 10000 samples each of size $n = 373$ using the model \mathcal{M} with parameters $p_0 = 0.5898$, $p_1 = 0.1555$, $p_2 = 0.1019$, $p_3 = 0.0965$, $p_4 = 0.0349$, $p_5 = 0.0134$, $p_6 = 0.008$ and p_7, p_8, \dots are all equal to 0. These specific values for the probabilities were chosen from the observed recruitment proportions in the SATHCAP dataset (Table 1). Using these 10000 samples, the inclusion probability of any individual in the population under the model \mathcal{M} (for the chosen parameters) can be well-approximated by the proportion of samples containing the individual. These inclusion probabilities are plotted against degrees for each of the two networks G_1 and G_2 in Figure 2. It is clear from Figure 2 that the inclusion probabilities for G_1 and G_2 are quite and meaningfully distinct (the scale of the two plots is exactly the same) even though G_1 and G_2 have identical degrees. The inclusion probabilities for individuals in G_1 are roughly proportional to the square root of their degrees. On the other hand, the inclusion probabilities in G_2 are nearly directly proportional to degrees. Therefore, the inclusion probabilities for the model \mathcal{M} depend not only the degrees but also on the network structure of the true population.

4. Conclusion and Future Work. In contrast with earlier works on respondent driven sampling, we presented a realistic RDS model, motivated by a real world RDS dataset. We demonstrated that for this model, the inclusion probabilities of sample individuals does not depend on their de-

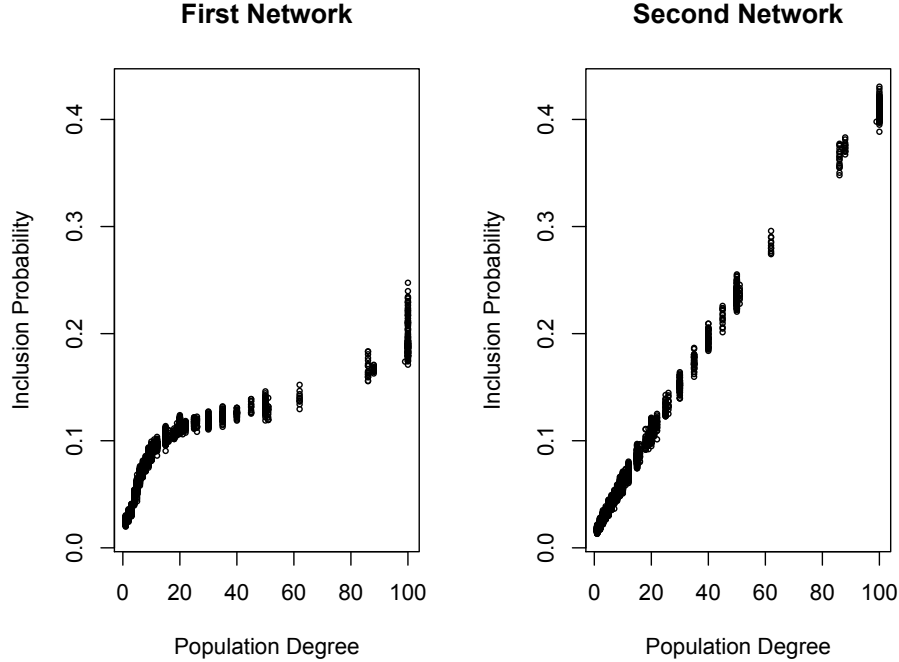


Fig 2: For each of the two networks G_1 and G_2 , the inclusion probabilities of all population individuals under the model \mathcal{M} are plotted against degrees. The scale is exactly the same in both the plots.

degrees alone. Indeed, we constructed two population networks G_1 and G_2 having identical set of nodes and degrees but with vastly different inclusion probabilities. This implies that, for this RDS model, it is impossible to construct a general estimation theory for population means based on the Horvitz-Thompson estimator.

For estimation under such a realistic RDS model to be feasible, we either need more information about the underlying population network or we need to be content in only estimating certain but not all population means. In this regard, we have the following ideas which we hope to explore in future work:

1. Under assumptions in Volz and Heckathorn (2008), the inclusion probabilities of sampled individuals are proportional to their degrees and hence they depend solely on the degrees up to the constant of proportionality. Heckathorn (1997) realized that the researcher can learn

the degrees of individuals by just asking them and since then, sampled individuals are always asked to report their degrees in RDS studies. In the case of the model \mathcal{M} however, we have seen that the inclusion probabilities depend not only on the degrees but also on the network structure of the true population. It is of interest to understand the precise network characteristics on which the inclusion probabilities depend and whether such characteristics can be learned by asking the sampled subjects additional questions. Recent work by Cepeda et al (2011) suggests that additional information on network structure such as total network size and stability would enhance HIV prevalence estimates and assist prevention measures in a population of injection drug users. These types of questions could yield enough information about the underlying network for the purpose of approximating inclusion probabilities.

2. We have studied two network models in this paper; the ones that were involved in the construction of G_1 and G_2 . It will be of interest to study more such network models and to investigate the behavior of inclusion probabilities under them.
3. It will be of interest to explore alternative RDS estimators that are not based on the Horvitz-Thompson estimator. Such estimators may not have the general applicability of the Horvitz-Thompson estimator but may work in certain special instances. For example, suppose that the population quantity whose mean we are interested in estimating is distributed as a Bernoulli random variable with probability of success equal to p and suppose that p is independent of all features of the network. In that case, it should be clear that the sample mean is as good as any other estimator. In other words, if the quantity of interest does not depend on the network features, then the sample mean is an adequate estimator. Drawing from this intuition, it is reasonable to believe that for population quantities that do not depend significantly on the degrees, one might not need to use the Horvitz-Thompson estimator as simpler estimates based perhaps on the sample mean might be adequate. Making such an idea rigorous will require more work.

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